L17 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1995:598165 CAPLUS
DN 123:48685
TI Rapid **mass spectrometric peptide** sequencing and **mass** matching for characterization of human melanoma **proteins** isolated by two-dimensional PAGE
AU Clauser, Karl R.; Hall, Steven C.; Smith, Diana M.; Webb, James W.; Andrews, Lori E.; Tran, Huu M.; Epstein, Lois B.; Burlingame, Alma L.
CS Dep. Pharmaceutical Chem., Univ. California, San Francisco, CA, 94143, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1995), 92(11), 5072-6
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 6
AB The authors report a general **mass spectrometric** approach for the rapid identification and characterization of **proteins** isolated by preparative two-dimensional polyacrylamide **gel** electrophoresis. This method possesses the inherent power to detect and structurally characterize covalent modifications. Abs. sensitivities of matrix-assisted laser desorption ionization and high-energy collision-induced dissocn. tandem **mass spectrometry** are exploited to det. the **mass** and sequence of subpicomole sample quantities of tryptic **peptides**. These data permit **mass** matching and sequence homol. searching of computerized **peptide mass** and **protein** sequence data bases for known **proteins** and design of oligonucleotide probes for cloning unknown **proteins**. The authors have identified 11 **proteins** in lysates of human A375 melanoma cells, including: .alpha.-enolase, cytokeratin, stathmin, **protein** disulfide isomerase, tropomyosin, Cu/Zn superoxide dismutase, nucleoside diphosphate kinase A, galaptin, and triosephosphate isomerase. The authors have characterized several **post-translation** modifications and chem. modifications that may result from electrophoresis or subsequent sample processing steps. Detection of comigrating and covalently modified **proteins** illustrates the necessity of **peptide** sequencing and the advantages of tandem **mass spectrometry** to reliably and unambiguously establish the identity of each **protein**. This technol. paves the way for studies of cell-type dependent gene expression and studies of large suites of cellular **proteins** with unprecedented speed and rigor to provide information complementary to the ongoing Human Genome Project.
ST PAGE human melanoma **protein** purifn method
IT **Proteins, specific** or class
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PUR (Purification or recovery); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation)
(melanoma-assocd.; rapid **mass spectrometric peptide** sequencing and **mass** matching for characterization of human melanoma **proteins** isolated by two-dimensional PAGE)
IT **Mass spectrometry**
Melanoma
(rapid **mass spectrometric peptide** sequencing and **mass** matching for characterization of human melanoma **proteins** isolated by two-dimensional PAGE)
IT Keratins
Tropomyosins
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PUR

(Purification or recovery); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation)
(rapid **mass spectrometric peptide** sequencing and **mass** matching for characterization of human melanoma **proteins** isolated by two-dimensional PAGE)

IT Agglutinins and Lectins
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PUR (Purification or recovery); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation)
(galaptins, rapid **mass spectrometric peptide** sequencing and **mass** matching for characterization of human melanoma **proteins** isolated by two-dimensional PAGE)

IT Electrophoresis and Ionophoresis
(**gel**, polyacrylamide; rapid **mass spectrometric peptide** sequencing and **mass** matching for characterization of human melanoma **proteins** isolated by two-dimensional PAGE)

IT Phosphoproteins
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PUR (Purification or recovery); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation)
(stathmins, rapid **mass spectrometric peptide** sequencing and **mass** matching for characterization of human melanoma **proteins** isolated by two-dimensional PAGE)

IT 9026-51-1P, Nucleoside diphosphate kinase
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PUR (Purification or recovery); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation)
(A; rapid **mass spectrometric peptide** sequencing and **mass** matching for characterization of human melanoma **proteins** isolated by two-dimensional PAGE)

IT 9014-08-8P
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PUR (Purification or recovery); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation)
(a-; rapid **mass spectrometric peptide** sequencing and **mass** matching for characterization of human melanoma **proteins** isolated by two-dimensional PAGE)

IT 9054-89-1P
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PUR (Purification or recovery); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation)
(copper-zinc-contg.; rapid **mass spectrometric peptide** sequencing and **mass** matching for characterization of human melanoma **proteins** isolated by two-dimensional PAGE)

IT 9023-78-3P, Triosephosphate isomerase 37318-49-3P, **Protein** disulfide isomerase
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PUR (Purification or recovery); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation)
(rapid **mass spectrometric peptide** sequencing and **mass** matching for characterization of human melanoma **proteins** isolated by two-dimensional PAGE)

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L9 ANSWER 9 OF 14 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
AN 2001:349283 BIOSIS
DN PREV200100349283
TI Rapid quantitative measurements of proteomes by Fourier transform ion cyclotron resonance **mass spectrometry**.
AU Smith, Richard D. (1); Pasa-Tolic, Ljiljana; Lipton, Mary S.; Jensen, Pamela K.; Anderson, Gordon A.; Shen, Yufeng; Conrads, Thomas P.; Udseth, Harold R.; Harkewicz, Richard; Belov, Mikhail E.; Masselon, Christophe; Veenstra, Timothy D.
CS (1) Environmental Molecular Sciences Laboratory, Pacific Northwest National Laboratory, Mail Stop K8-98, Richland, WA, 99352: rd_smith@pnl.gov USA
SO Electrophoresis, (May, 2001) Vol. 22, No. 9, pp. 1652-1668. print. ISSN: 0173-0835.
DT Article
LA English
SL English
AB The patterns of gene expression, post-translational modifications, **protein**/biomolecular interactions, and how these may be affected by changes in the environment, cannot be accurately predicted from DNA sequences. Approaches for proteome characterization are generally based upon mass spectrometric analysis of in-gel digested two dimensional polyacrylamide **gel electrophoresis** (2-D PAGE) separated **proteins**, allowing relatively rapid **protein** identification compared to conventional approaches. This technique, however, is constrained by the speed of the 2-D PAGE separations, the sensitivity limits intrinsic to staining necessary for **protein** visualization, the speed and sensitivity of subsequent mass spectrometric analyses for identification, and the limited ability for accurate quantitative measurements based on differences in spot intensity. We are presently developing alternative approaches for proteomics based upon the combination of fast capillary electrophoresis, or other suitable chromatographic separations, and the high mass accuracy and sensitivity obtainable with unique Fourier transform ion cyclotron resonance (FTICR) mass spectrometers available at our laboratory. Several approaches are presently being pursued; one based upon the analysis of intact **proteins** and the second upon approaches for global **protein** **digestion** and accurate peptide mass analysis. Quantitation of **protein**/peptide levels are based on using two or more stable-**isotope** labeled versions of proteomes which are combined to obtain precise quantitation of relative **protein** abundances. We describe the status of our efforts towards the development of a high-throughput proteomics capability and present initial results for application to several microorganisms and discuss our efforts for extending the developed capability to mammalian proteomes.
CC Biochemical Studies - General *10060
IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques
IT Chemicals & Biochemicals
proteomes: rapid quantitative measurements
IT Methods & Equipment
7 tesla ESI-FTICR mass spectrometer: Finnigan, laboratory equipment; Fourier transform ion cyclotron resonance **mass** **spectrometry**: analytical method, spectroscopic techniques: CB; two dimensional polyacrylamide **gel electrophoresis**: analytical method, **gel electrophoresis**

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Biochemistry and Molecular Biophysics; Methods and Techniques
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proteomes: rapid quantitative measurements
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7 tesla ESI-FTICR mass spectrometer: Finnigan, laboratory equipment; Fourier transform ion cyclotron resonance **mass** **spectrometry**: analytical method, spectroscopic techniques: CB; two dimensional polyacrylamide **gel electrophoresis**: analytical method, **gel electrophoresis**